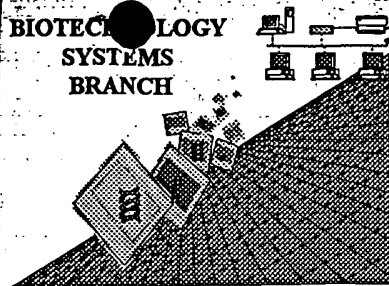


*Yuck*

## RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



#9

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/115,589

Source: 1647

Date Processed by STIC: 6/30/2000

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY  
EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/11/99, 589

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☒ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ☐ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ☐ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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S. Gucker

1647

RAW SEQUENCE LISTING      DATE: 07/07/2000  
 PATENT APPLICATION: US/09/115,589      TIME: 09:34:34

Input Set : A:\Muscdaml.app  
 Output Set: N:\CRF3\07072000\I115589.raw

3 <110> APPLICANT: Van Eyk, Jennifer E.  
 4 Iscoe, Steven D  
 5 Simpson, Jeremy A  
 7 <120> TITLE OF INVENTION: Methods of Diagnosing Muscle Damage  
 9 <130> FILE REFERENCE: 1997-023-02US  
 11 <140> CURRENT APPLICATION NUMBER: 09/115,589  
 12 <141> CURRENT FILING DATE: 1998-07-15  
 14 <150> PRIOR APPLICATION NUMBER: 60/052,697  
 15 <151> PRIOR FILING DATE: 1997-07-16  
 17 <160> NUMBER OF SEQ ID NOS: 18  
 19 <170> SOFTWARE: PatentIn Ver. 2.1  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 12  
 23 <212> TYPE: PRT  
 24 <213> ORGANISM: Unknown  
 26 <220> FEATURE:  
 27 <221> NAME/KEY: PEPTIDE  
 28 <222> LOCATION: (1)..(12)  
 29 <223> OTHER INFORMATION: Myosin light chain 1  
 31 <220> FEATURE:  
 32 <221> NAME/KEY: PEPTIDE  
 33 <222> LOCATION: (7)  
 34 <223> OTHER INFORMATION: May be either Pro or Ala  
 36 <400> SEQUENCE: 1  
 W--> 37 Xaa Xaa Lys Lys Pro Glu Xaa Lys Ala Asp Asp Ala  
 38 1 5 10  
 41 <210> SEQ ID NO: 2  
 42 <211> LENGTH: 12  
 43 <212> TYPE: PRT  
 44 <213> ORGANISM: Unknown  
 46 <220> FEATURE:  
 47 <221> NAME/KEY: PEPTIDE  
 48 <222> LOCATION: (1)..(12)  
 49 <223> OTHER INFORMATION: Myosin light chain 1  
 51 <400> SEQUENCE: 2  
 W--> 52 Xaa Pro Ala Pro Ala Ala Pro Ala Ala Ala Pro  
 53 1 5 10  
 56 <210> SEQ ID NO: 3  
 57 <211> LENGTH: 11  
 58 <212> TYPE: PRT  
 59 <213> ORGANISM: Unknown  
 61 <220> FEATURE:  
 62 <221> NAME/KEY: PEPTIDE  
 63 <222> LOCATION: (1)..(11)  
 64 <223> OTHER INFORMATION: malate dehydrogenase  
 66 <400> SEQUENCE: 3  
 W--> 67 Xaa Lys Val Ala Leu Gly Ala Xaa Gly Gly Ile

Does Not Comply  
 Corrected Diskette Needed

pp 1-2

what about Xaa's at locations  
 1 and 2?

see item 10 on Even Summary Sheet

item 10

## RAW SEQUENCE LISTING

DATE: 07/07/2000

PATENT APPLICATION: US/09/115,589

TIME: 09:34:34

Input Set : A:\Muscdaml.app

Output Set: N:\CRF3\07072000\I115589.raw

68 1 5 10  
71 <210> SEQ ID NO: 4  
72 <211> LENGTH: 13  
73 <212> TYPE: PRT  
74 <213> ORGANISM: Unknown  
76 <220> FEATURE:  
77 <221> NAME/KEY: PEPTIDE  
78 <222> LOCATION: (1)..(13)  
79 <223> OTHER INFORMATION: ATP g synthase chain  
81 <400> SEQUENCE: 4  
W--> 82 Xaa Xaa Leu Lys Asp Ile Thr Arg Arg Leu Lys Ser Ile  
83 1 5 10  
86 <210> SEQ ID NO: 5  
87 <211> LENGTH: 10  
88 <212> TYPE: PRT  
89 <213> ORGANISM: Unknown  
91 <220> FEATURE:  
92 <221> NAME/KEY: PEPTIDE  
93 <222> LOCATION: (1)..(10)  
94 <223> OTHER INFORMATION: ATP synthase oligomycin conferring protein  
96 <400> SEQUENCE: 5  
W--> 97 Xaa Xaa Lys Leu Val Arg Pro Pro Val Gln  
98 1 5 10  
101 <210> SEQ ID NO: 6  
102 <211> LENGTH: 10  
103 <212> TYPE: PRT  
104 <213> ORGANISM: Unknown  
106 <220> FEATURE:  
107 <221> NAME/KEY: PEPTIDE  
108 <222> LOCATION: (1)..(10)  
109 <223> OTHER INFORMATION: serum albumin  
111 <400> SEQUENCE: 6  
W--> 112 Xaa Ala His Lys Ser Glu Ile Ala His Arg  
113 1 5 10  
116 <210> SEQ ID NO: 7  
117 <211> LENGTH: 11  
118 <212> TYPE: PRT  
119 <213> ORGANISM: Unknown  
121 <220> FEATURE:  
122 <221> NAME/KEY: PEPTIDE  
123 <222> LOCATION: (4)  
124 <223> OTHER INFORMATION: May be Arg or Leu  
126 <220> FEATURE:  
127 <221> NAME/KEY: PEPTIDE  
128 <222> LOCATION: (1)..(11)  
129 <223> OTHER INFORMATION: triose phosphate isomerase  
131 <400> SEQUENCE: 7  
W--> 132 Xaa Pro Ser Xaa Lys Phe Phe Val Gly Gly Asn  
133 1 5 10

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RAW SEQUENCE LISTING                      DATE: 07/07/2000  
 PATENT APPLICATION:    US/09/115,589        TIME: 09:34:34

Input Set : A:\Muscdaml.app  
 Output Set: N:\CRF3\07072000\I115589.raw

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136 <210> SEQ ID NO: 8
137 <211> LENGTH: 209
138 <212> TYPE: PRT
139 <213> ORGANISM: Unknown
141 <220> FEATURE:
142 <221> NAME/KEY: PEPTIDE
143 <222> LOCATION: (1)..(209)
144 <223> OTHER INFORMATION: Human cardiac troponin I
146 <220> FEATURE:
147 <223> OTHER INFORMATION: Swiss prot identification number P19429
149 <300> PUBLICATION INFORMATION:
150 <303> JOURNAL: FEBS Lett.
151 <304> VOLUME: 270
152 <306> PAGES: 57-61
153 <307> DATE: 1990
155 <400> SEQUENCE: 8
156 Ala Asp Gly Ser Ser Asp Ala Ala Arg Glu Pro Arg Pro Ala Pro Ala
157   1           5           10           15
159 Pro Ile Arg Arg Arg Ser Ser Asn Tyr Arg Ala Tyr Ala Thr Glu Pro
160   20           25           30
162 His Ala Lys Lys Lys Ser Lys Ile Ser Ala Ser Arg Lys Leu Gln Leu
163   35           40           45
165 Lys Thr Leu Leu Leu Gln Ile Ala Lys Gln Glu Leu Arg Glu Ala
166   50           55           60
168 Glu Glu Arg Arg Gly Glu Lys Gly Arg Ala Leu Ser Thr Arg Cys Gln
169   65           70           75           80
171 Pro Leu Glu Leu Ala Gly Leu Gly Phe Ala Glu Leu Gln Asp Leu Cys
172   85           90           95
174 Arg Gln Leu His Ala Arg Val Asp Lys Val Asp Glu Glu Arg Tyr Asp
175   100          105          110
177 Ile Glu Ala Lys Val Thr Lys Asn Ile Thr Glu Ile Ala Asp Leu Thr
178   115          120          125
180 Gln Lys Ile Phe Asp Leu Arg Gly Lys Phe Lys Arg Pro Thr Leu Arg
181   130          135          140
183 Arg Val Arg Ile Ser Ala Asp Ala Met Met Gln Ala Leu Leu Gly Ala
184   145          150          155          160
186 Arg Ala Lys Glu Ser Leu Asp Leu Arg Ala His Leu Lys Gln Val Lys
187   165          170          175
189 Lys Glu Asp Thr Glu Lys Glu Asn Arg Glu Val Gly Asp Trp Arg Lys
190   180          185          190
192 Asn Ile Asp Ala Leu Ser Gly Met Glu Gly Arg Lys Lys Phe Glu
193   195          200          205
195 Ser
199 <210> SEQ ID NO: 9
200 <211> LENGTH: 186
201 <212> TYPE: PRT
202 <213> ORGANISM: Unknown
204 <220> FEATURE:
205 <221> NAME/KEY: PEPTIDE

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RAW SEQUENCE LISTING                      DATE: 07/07/2000  
 PATENT APPLICATION:    US/09/115,589        TIME: 09:34:35

Input Set : A:\Muscdaml.app  
 Output Set: N:\CRF3\07072000\I115589.raw

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206 <222> LOCATION: (1)..(186)
207 <223> OTHER INFORMATION: Human slow skeletal troponin I
209 <220> FEATURE:
210 <223> OTHER INFORMATION: Swiss prot identification number P19237
212 <300> PUBLICATION INFORMATION:
213 <303> JOURNAL: Genomics
214 <304> VOLUME: 7
215 <306> PAGES: 346-357
216 <307> DATE: 1990
218 <400> SEQUENCE: 9
219 Pro Glu Val Glu Arg Lys Pro Lys Ile Thr Ala Ser Arg Lys Leu Leu
220   1           5           10           15
222 Leu Lys Ser Leu Met Leu Ala Lys Ala Lys Glu Cys Trp Glu Gln Glu
223           20           25           30
225 His Glu Glu Arg Glu Ala Glu Lys Val Arg Tyr Leu Ala Glu Arg Ile
226           35           40           45
228 Pro Thr Leu Gln Thr Arg Gly Leu Ser Leu Ser Ala Leu Gln Asp Leu
229   50           55           60
231 Cys Arg Glu Leu His Ala Lys Val Glu Val Val Asp Glu Glu Arg Tyr
232   65           70           75           80
234 Asp Ile Glu Ala Lys Cys Leu His Asn Thr Arg Glu Ile Lys Asp Leu
235           85           90           95
237 Lys Leu Lys Val Met Asp Leu Arg Gly Lys Phe Lys Arg Pro Pro Leu
238           100          105          110
240 Arg Arg Val Arg Val Ser Ala Asp Ala Met Leu Arg Ala Leu Leu Gly
241           115          120          125
243 Ser Lys His Lys Val Ser Met Asp Leu Arg Ala Asn Leu Lys Ser Val
244           130          135          140
246 Lys Lys Glu Asp Thr Glu Lys Glu Arg Pro Val Glu Val Gly Asp Trp
247 145           150           155           160
249 Arg Lys Asn Val Glu Ala Met Ser Gly Met Glu Gly Arg Lys Lys Met
250           165           170           175
252 Phe Asp Ala Ala Lys Ser Pro Thr Ser Gln
253           180           185
256 <210> SEQ ID NO: 10
257 <211> LENGTH: 181
258 <212> TYPE: PRT
259 <213> ORGANISM: Unknown
261 <220> FEATURE:
262 <221> NAME/KEY: PEPTIDE
263 <222> LOCATION: (1)..(181)
264 <223> OTHER INFORMATION: Human fast skeletal troponin I
266 <220> FEATURE:
267 <223> OTHER INFORMATION: Swiss prot identification number P48788
269 <300> PUBLICATION INFORMATION:
270 <303> JOURNAL: Biochim. Biophys. Acta
271 <304> VOLUME: 1217
272 <306> PAGES: 338-340
-> 273 <307> DATE: 1994

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RAW SEQUENCE LISTING                      DATE: 07/07/2000  
 PATENT APPLICATION:    US/09/115,589        TIME: 09:34:35

Input Set : A:\Muscdaml.app  
 Output Set: N:\CRF3\07072000\I115589.raw

```

275 <400> SEQUENCE: 10
276 Gly Asp Glu Glu Lys Arg Asn Arg Ala Ile Thr Ala Arg Arg Gln His
277   1           5           10           15
279 Leu Lys Ser Val Met Leu Gln Ile Ala Ala Thr Glu Leu Glu Lys Glu
280           20           25           30
282 Glu Ser Arg Arg Glu Ala Glu Lys Gln Asn Tyr Leu Ala Glu His Cys
283   35           40           45
285 Pro Pro Leu His Ile Pro Gly Ser Met Ser Glu Val Gln Glu Leu Cys
286   50           55           60
288 Lys Gln Leu His Ala Lys Ile Asp Ala Ala Glu Glu Lys Tyr Asp
289   65           70           75           80
291 Met Glu Val Arg Val Gln Lys Thr Ser Lys Glu Leu Glu Asp Met Asn
292           85           90           95
294 Gln Lys Leu Phe Asp Leu Arg Gly Lys Phe Lys Arg Pro Pro Leu Arg
295           100          105          110
297 Arg Val Arg Met Ser Ala Asp Ala Met Leu Lys Ala Leu Leu Gly Ser
298           115          120          125
300 Lys His Lys Val Cys Met Asp Leu Arg Ala Asn Leu Lys Gln Val Lys
301           130          135          140
303 Lys Glu Asp Thr Glu Lys Glu Arg Asp Leu Arg Asp Val Gly Asp Trp
304 145           150          155          160
306 Arg Lys Asn Ile Glu Glu Lys Ser Gly Met Glu Gly Arg Lys Lys Met
307           165          170          175
309 Phe Glu Ser Glu Ser
310           180
313 <210> SEQ ID NO: 11
314 <211> LENGTH: 210
315 <212> TYPE: PRT
316 <213> ORGANISM: Unknown
318 <220> FEATURE:
319 <221> NAME/KEY: PEPTIDE
320 <222> LOCATION: (1)..(210)
321 <223> OTHER INFORMATION: Rat cardiac troponin I
323 <220> FEATURE:
324 <223> OTHER INFORMATION: Swiss prot identification number P23693
326 <300> PUBLICATION INFORMATION:
327 <303> JOURNAL: Biochemistry
328 <304> VOLUME: 30
329 <306> PAGES: 707-712
330 <307> DATE: 1991
332 <400> SEQUENCE: 11
333 Ala Asp Glu Ser Ser Asp Ala Ala Gly Glu Pro Gln Pro Ala Pro Ala
334   1           5           10           15
336 Pro Val Arg Arg Arg Ser Ser Ala Asn Tyr Arg Ala Tyr Ala Thr Glu
337           20           25           30
339 Pro His Ala Lys Lys Lys Ser Lys Ile Ser Ala Ser Arg Lys Leu Gln
340           35           40           45
342 Leu Lys Thr Leu Met Leu Gln Ile Ala Lys Gln Glu Met Glu Arg Glu
343           50           55           60

```

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/115,589

DATE: 07/07/2000

TIME: 09:34:36

Input Set : A:\Muscdaml.app

Output Set: N:\CRF3\07072000\I115589.raw

L:37 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:67 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:82 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:97 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:112 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:153 M:285 W: Invalid Journal Date: Wrong YYYY-MM-DD,MMM-YYYY or SEASON-YYYY, Wrong Journal Date:YYYY-MM-DD,MMM-YYYY or Season-YYYY  
L:216 M:285 W: Invalid Journal Date: Wrong YYYY-MM-DD,MMM-YYYY or SEASON-YYYY, Wrong Journal Date:YYYY-MM-DD,MMM-YYYY or Season-YYYY  
L:273 M:285 W: Invalid Journal Date: Wrong YYYY-MM-DD,MMM-YYYY or SEASON-YYYY, Wrong Journal Date:YYYY-MM-DD,MMM-YYYY or Season-YYYY  
L:330 M:285 W: Invalid Journal Date: Wrong YYYY-MM-DD,MMM-YYYY or SEASON-YYYY, Wrong Journal Date:YYYY-MM-DD,MMM-YYYY or Season-YYYY  
L:393 M:285 W: Invalid Journal Date: Wrong YYYY-MM-DD,MMM-YYYY or SEASON-YYYY, Wrong Journal Date:YYYY-MM-DD,MMM-YYYY or Season-YYYY  
L:504 M:285 W: Invalid Journal Date: Wrong YYYY-MM-DD,MMM-YYYY or SEASON-YYYY, Wrong Journal Date:YYYY-MM-DD,MMM-YYYY or Season-YYYY  
L:579 M:285 W: Invalid Journal Date: Wrong YYYY-MM-DD,MMM-YYYY or SEASON-YYYY, Wrong Journal Date:YYYY-MM-DD,MMM-YYYY or Season-YYYY  
L:654 M:285 W: Invalid Journal Date: Wrong YYYY-MM-DD,MMM-YYYY or SEASON-YYYY, Wrong Journal Date:YYYY-MM-DD,MMM-YYYY or Season-YYYY  
L:726 M:285 W: Invalid Journal Date: Wrong YYYY-MM-DD,MMM-YYYY or SEASON-YYYY, Wrong Journal Date:YYYY-MM-DD,MMM-YYYY or Season-YYYY  
L:804 M:285 W: Invalid Journal Date: Wrong YYYY-MM-DD,MMM-YYYY or SEASON-YYYY, Wrong Journal Date:YYYY-MM-DD,MMM-YYYY or Season-YYYY